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## RAW SEQUENCE LISTING

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Application Serial Number: 10/511,468  
Source: PCT  
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PCT

## RAW SEQUENCE LISTING

DATE: 01/17/2006

PATENT APPLICATION: US/10/511,468

TIME: 11:26:46

Input Set : A:\2005-11-21 4614-0159PUS1.ST25.txt

Output Set: N:\CRF4\01172006\J511468.raw

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5 <110> APPLICANT: Soren Weis DAHL et al.
7 <120> TITLE OF INVENTION: TRANSLOCATION DEPENDENT COMPLEMENTATION FOR DRUG SCREENING
9 <130> FILE REFERENCE: 4614-0159PUS1
11 <140> CURRENT APPLICATION NUMBER: US 10/511,468
12 <141> CURRENT FILING DATE: 2004-10-18
14 <160> NUMBER OF SEQ ID NOS: 99
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 238
20 <212> TYPE: PRT
21 <213> ORGANISM: Aequorea victoria
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27 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
28 20 25 30
30 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
31 35 40 45
33 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
34 50 55 60
36 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
37 65 70 75 80
39 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
40 85 90 95
42 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
43 100 105 110
45 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
46 115 120 125
48 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
49 130 135 140
51 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
52 145 150 155 160
54 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
55 165 170 175
57 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
58 180 185 190
60 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
61 195 200 205
63 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
64 210 215 220
66 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
67 225 230 235
69 <210> SEQ ID NO: 2

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70 &lt;211&gt; LENGTH: 238

71 &lt;212&gt; TYPE: PRT

72 &lt;213&gt; ORGANISM: Aequorea victoria

74 &lt;400&gt; SEQUENCE: 2

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75 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
76 1          5          10          15
78 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
79          20          25          30
81 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
82          35          40          45
84 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
85          50          55          60
87 Ser Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
88 65          70          75          80
90 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
91          85          90          95
93 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
94          100          105          110
96 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
97          115          120          125
99 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
100          130          135          140
102 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
103 145          150          155          160
105 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
106          165          170          175
108 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
109          180          185          190
111 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
112          195          200          205
114 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
115          210          215          220
117 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
118 225          230          235

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120 &lt;210&gt; SEQ ID NO: 3

121 &lt;211&gt; LENGTH: 238

122 &lt;212&gt; TYPE: PRT

123 &lt;213&gt; ORGANISM: Aequorea victoria

125 &lt;400&gt; SEQUENCE: 3

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126 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
127 1          5          10          15
129 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
130          20          25          30
132 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
133          35          40          45
135 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
136          50          55          60
138 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
139 65          70          75          80

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141 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
142      85      90      95
144 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
145      100     105     110
147 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
148      115     120     125
150 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
151      130     135     140
153 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
154 145      150     155     160
156 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
157      165     170     175
159 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
160      180     185     190
162 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
163      195     200     205
165 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
166      210     215     220
168 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
169 225      230     235
171 <210> SEQ ID NO: 4
172 <211> LENGTH: 239
173 <212> TYPE: PRT
174 <213> ORGANISM: Aequorea victoria
176 <400> SEQUENCE: 4
177 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
178 1      5      10      15
180 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
181      20      25      30
183 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
184      35      40      45
186 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
187      50      55      60
189 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
190 65      70      75      80
192 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
193      85      90      95
195 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
196      100     105     110
198 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
199      115     120     125
201 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
202      130     135     140
204 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
205 145      150     155     160
207 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
208      165     170     175
210 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
211      180     185     190

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213 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
214          195          200          205
216 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
217          210          215          220
219 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
220 225          230          235
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 239
224 <212> TYPE: PRT
225 <213> ORGANISM: Aequorea victoria
227 <400> SEQUENCE: 5
228 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
229 1          5          10          15
231 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
232          20          25          30
234 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
235          35          40          45
237 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
238          50          55          60
240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
241 65          70          75          80
243 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
244          85          90          95
246 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
247          100         105         110
249 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
250          115         120         125
252 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
253          130         135         140
255 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
256 145         150         155         160
258 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
259          165         170         175
261 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
262          180         185         190
264 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
265          195         200         205
267 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
268          210         215         220
270 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
271 225         230         235
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 239
275 <212> TYPE: PRT
276 <213> ORGANISM: Aequorea victoria
278 <400> SEQUENCE: 6
279 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
280 1          5          10          15
282 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

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283          20          25          30
285 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
286          35          40          45
288 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
289          50          55          60
291 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
292 65          70          75          80
294 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
295          85          90          95
297 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
298          100         105         110
301 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
302          115         120         125
304 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
305          130         135         140
307 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
308 145          150         155         160
310 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
311          165         170         175
313 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
314          180         185         190
316 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
317          195         200         205
319 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
320          210         215         220
322 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
323 225          230         235
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328 <212> TYPE: DNA
329 <213> ORGANISM: Homo sapiens
331 <220> FEATURE:
332 <221> NAME/KEY: CDS
333 <222> LOCATION: (3)..(116)
335 <400> SEQUENCE: 7
336 cc atg gcc ggt ggt acc ggt tcc ggt gcc ctg aag aag gag ctg cag      47
337 Met Ala Gly Gly Thr Gly Ser Gly Ala Leu Lys Lys Glu Leu Gln
338 1          5          10          15
340 gcc aac aag aag gag ctg gcc cag ctg aag tgg gag ctg cag gcc ctg      95
341 Ala Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu
342          20          25          30
344 aag aag gag ctg gcc cag tag gatcc      121
345 Lys Lys Glu Leu Ala Gln
346          35
348 <210> SEQ ID NO: 8
349 <211> LENGTH: 37
350 <212> TYPE: PRT
351 <213> ORGANISM: Homo sapiens
353 <400> SEQUENCE: 8

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**VERIFICATION SUMMARY**

DATE: 01/17/2006

PATENT APPLICATION: US/10/511,468

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